



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: US 09 840 243A
Source: OIPB
Date Processed by STIC: 10/22/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/940243A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length.
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/840,243A

TIME: 13:29:31

Input Set : A:\B3991AB_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

3 <110> APPLICANT: NOVIMMUNE SA
5 <120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
6 SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION
7 FACTOR AND MEDICAL USES OF THESE SUBSTANCES
9 <130> FILE REFERENCE: B3991AB-CS/KR
11 <140> CURRENT APPLICATION NUMBER: US/09/840,243A
12 <141> CURRENT FILING DATE: 2001-04-24
14 <150> PRIOR APPLICATION NUMBER: 98120085.0
15 <151> PRIOR FILING DATE: 1998-10-24
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 40
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
29 <400> SEQUENCE: 1
30 ccgtacgcgt ctagaccatg gagcttacc agcctgcaga 40
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 31
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
41 <400> SEQUENCE: 2
42 ttcgaattct cgagtgtctg agtccccggc a 31
45 <210> SEQ ID NO: 3
46 <211> LENGTH: 37
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial Sequence
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
53 <400> SEQUENCE: 3
54 ccgtacgcgt ctagaccatg gagccactc aggttgc 37
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 32
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
65 <400> SEQUENCE: 4
66 ttcgaattct cgagtgcctg gggtccagca gg
69 <210> SEQ ID NO: 5
70 <211> LENGTH: 30
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence

32. Error
check diskette

RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/840,243A

TIME: 13:29:31

Input Set : A:\B3991AB_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

```

74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
77 <400> SEQUENCE: 5
78 ccagctctag actccaccac tctcaccaac 30
81 <210> SEQ ID NO: 6
82 <211> LENGTH: 30
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
89 <400> SEQUENCE: 6
90 ccttcgaatt ctogctcttt tgccaggatg 30
93 <210> SEQ ID NO: 7
94 <211> LENGTH: 30
95 <212> TYPE: DNA
96 <213> ORGANISM: Artificial Sequence
98 <220> FEATURE:
99 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
101 <400> SEQUENCE: 7
102 ggttctctag attggcagca ctggggatag 30
105 <210> SEQ ID NO: 8
106 <211> LENGTH: 30
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
113 <400> SEQUENCE: 8
114 gctacgaatt ccagcagaca cagccaaaac 30
117 <210> SEQ ID NO: 9
118 <211> LENGTH: 69
119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
125 <400> SEQUENCE: 9
126 ccgtacgcgt ctagaatgga ttacaaagac gatgacgata agatggagct taccagcct 60
128 gcagaagac 69
131 <210> SEQ ID NO: 10
132 <211> LENGTH: 1345
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (418)..(1200)
140 <400> SEQUENCE: 10
141 acgcagggaa ggaggcacac ccgggggtgg cgcagtgagg agggggcgcg acggccagga 60
143 ggctggtgga gcgacacca ggcaggagag ggggaagaac tctctccctt tctgaacccc 120
145 cttttccttg agagacgagt tgggggagtc ctccacgcat taccactcg ggccgcaaaa 180
147 actcccttct ttagccctct gcccccgccc ttgcttataa gcctttgaga ccgcagaagg 240

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TIME: 13:29:31

Input Set : A:\B3991AB_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

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149 gaccttggtg tggaacggga cggccaagag gaagccagat cgctgagggt ccggtctcca 300
151 gtttgctcc tgctatatcc attggaagag aaaagtttgt gacttgggcc cccaagtttt 360
153 gagagaactg ggctttcggc gcgggggggac agaggaggct cgtggggagc ttcccc 417
155 atg gag ctt acc cag cct gca gaa gac ctc atc cag acc cag cag acc 465
156 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
157 1 5 10 15
159 cct gcc tca gaa ctt ggg gac cct gaa gac ccc gga gag gag gct gca 513
160 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
161 20 25 30
163 gat ggc tca gac act gtg gtc ctc agt ctc ttt ccc tgc acc cct gag 561
164 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
165 35 40 45
167 cct gtg aat cct gaa ccg gat gcc agt gtt tcc tct cca cag gca ggc 609
168 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
169 50 55 60
171 agc tcc ctg aag cac tcc acc act ctc acc aac cgg cag cga ggg aac 657
172 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
173 65 70 75 80
175 gag gtg tca gct ctg ccg gcc acc cta gac tcc ctg tcc atc cac cag 705
176 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
177 85 90 95
179 ctc gca gca cag ggg gag ctg gac cag ctg aag gag cat ttg cgg aaa 753
180 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
181 100 105 110
183 ggt gac aac ctc gtc aac aag cca gac gag cgc ggc ttc acc ccc ctc 801
184 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
185 115 120 125
187 atc tgg gcc tcc gcc ttt gga gag att gag acc gtt cgc ttc ctg ctg 849
188 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
189 130 135 140
191 gag tgg ggt gcc gac ccc cac atc ctg gca aaa gag cga gag agc gcc 897
192 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
193 145 150 155 160
195 ctg tcg ctg gcc agc aca ggc ggc tac aca gac att gtg ggg ctg ctg 945
196 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
197 165 170 175
199 ctg gag cgt gac gtg gac atc aac atc tat gat tgg aat gga ggg acg 993
200 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
201 180 185 190
203 cca ctg ctg tac gct gtg cgc ggg aac cac gtg aaa tgc gtt gag gcc 1041
204 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
205 195 200 205
207 ttg ctg gcc cga ggc gct gac ctc acc acc gaa gcc gac tct ggc tac 1089
208 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
209 210 215 220
211 acc ccg atg gac ctt gcc gtg gcc ctg gga tac cgg aaa gtg caa cag 1137
212 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
213 225 230 235 240
215 gtg atc gag aac cac atc ctc aag ctc ttc cag agc aac ctg gtg ccc 1185

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```

216 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
217           245           250           255
219 gct gac cct gag tga aggccgcctg ccgggggactc agacactcag ggaacaaaat 1240
220 Ala Asp Pro Glu
221           260
223 ggtcagccag agctggggaa acccagaact gacttcaaag gcagcttctg gacagggtggt 1300
225 gggaggggac ccttcccaag aggaaccaat aaaccttctg tgcag 1345
228 <210> SEQ ID NO: 11
229 <211> LENGTH: 260
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
233 <400> SEQUENCE: 11
234 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
235   1           5           10           15
237 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
238           20           25           30
240 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
241           35           40           45
243 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
244           50           55           60
246 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
247   65           70           75           80
249 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
250           85           90           95
252 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
253           100          105          110
255 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
256           115          120          125
258 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
259           130          135          140
261 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
262 145           150          155          160
264 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
265           165          170          175
267 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
268           180          185          190
270 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
271           195          200          205
273 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
274           210          215          220
276 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
277 225           230          235          240
279 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
280           245          250          255
282 Ala Asp Pro Glu
283           260
292 <210> SEQ ID NO: 12
293 <211> LENGTH: 260
294 <212> TYPE: PRT

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Input Set : A:\B3991AB_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

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295 <213> ORGANISM: Homo sapiens
297 <400> SEQUENCE: 12
298 Met Glu Leu Thr Gln Pro Ala Glu Asp Leu Ile Gln Thr Gln Gln Thr
299   1           5           10           15
301 Pro Ala Ser Glu Leu Gly Asp Pro Glu Asp Pro Gly Glu Glu Ala Ala
302           20           25           30
304 Asp Gly Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Glu
305           35           40           45
307 Pro Val Asn Pro Glu Pro Asp Ala Ser Val Ser Ser Pro Gln Ala Gly
308           50           55           60
310 Ser Ser Leu Lys His Ser Thr Thr Leu Thr Asn Arg Gln Arg Gly Asn
311   65           70           75           80
313 Glu Val Ser Ala Leu Pro Ala Thr Leu Asp Ser Leu Ser Ile His Gln
314           85           90           95
316 Leu Ala Ala Gln Gly Glu Leu Asp Gln Leu Lys Glu His Leu Arg Lys
317           100          105          110
319 Gly Asp Asn Leu Val Asn Lys Pro Asp Glu Arg Gly Phe Thr Pro Leu
320           115          120          125
322 Ile Trp Ala Ser Ala Phe Gly Glu Ile Glu Thr Val Arg Phe Leu Leu
323           130          135          140
325 Glu Trp Gly Ala Asp Pro His Ile Leu Ala Lys Glu Arg Glu Ser Ala
326   145          150          155          160
328 Leu Ser Leu Ala Ser Thr Gly Gly Tyr Thr Asp Ile Val Gly Leu Leu
329           165          170          175
331 Leu Glu Arg Asp Val Asp Ile Asn Ile Tyr Asp Trp Asn Gly Gly Thr
332           180          185          190
334 Pro Leu Leu Tyr Ala Val Arg Gly Asn His Val Lys Cys Val Glu Ala
335           195          200          205
337 Leu Leu Ala Arg Gly Ala Asp Leu Thr Thr Glu Ala Asp Ser Gly Tyr
338           210          215          220
340 Thr Pro Met Asp Leu Ala Val Ala Leu Gly Tyr Arg Lys Val Gln Gln
341   225          230          235          240
343 Val Ile Glu Asn His Ile Leu Lys Leu Phe Gln Ser Asn Leu Val Pro
344           245          250          255
346 Ala Asp Pro Glu
347           260
350 <210> SEQ ID NO: 13
351 <211> LENGTH: 269
352 <212> TYPE: PRT
353 <213> ORGANISM: Murinae gen. sp.
355 <400> SEQUENCE: 13
356 Met Glu Pro Thr Gln Val Ala Glu Asn Leu Val Pro Asn Gln Gln Pro
357   1           5           10           15
359 Pro Val Pro Asp Leu Glu Asp Pro Glu Asp Thr Arg Asp Glu Ser Pro
360           20           25           30
362 Glu Asn Ser Asp Thr Val Val Leu Ser Leu Phe Pro Cys Thr Pro Asp
363           35           40           45
365 Ala Val Asn Pro Glu Ala Asp Ala Ser Ala Ser Ser Leu Gln Gly Ser
366           50           55           60

```

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

<210> SEQ ID NO 18
<211> LENGTH: 220
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: 31
<221> NAME/KEY: UNSURE
<222> LOCATION: 148
<221> NAME/KEY: UNSURE
<222> LOCATION: 159
<400> SEQUENCE: 18

12:30 pm 11/07/01

Sequence listing as of
the above time and date.

Field 223 is required
to enumerate unknown Xaa's
and possible values

VERIFICATION SUMMARY

DATE: 10/29/2001

PATENT APPLICATION: US/09/840,243A

TIME: 13:29:32

Input Set : A:\B3991AB_SQL.txt

Output Set: N:\CRF3\10292001\I840243A.raw

L:496 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18

L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18

L:520 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18

L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18